

In the **Specification**, please enter the following amendments.

On page 18, before the first full paragraph starting with “Enzymes possessing 3’-5’ exonuclease activity” and ends with “Preferably, the enzyme comprising 3’-5’ exonuclease activity is a DNA polymerase,” please add the following text:

--Amino acid sequence of JDF-3 DNA polymerase (Sequence 2 of WO 01/32887):

Met	Ile	Leu	Asp	Val	Asp	Tyr	Ile	Thr	Glu	Asn	Gly	Lys	Pro	Val	Ile
1				5						10				15	
Arg	Val	Phe	Lys	Lys	Glu	Asn	Gly	Glu	Phe	Arg	Ile	Glu	Tyr	Asp	Arg
				20						25				30	
Glu	Phe	Glu	Pro	Tyr	Phe	Tyr	Ala	Leu	Leu	Arg	Asp	Asp	Ser	Ala	Ile
				35						40				45	
Glu	Glu	Ile	Lys	Lys	Ile	Thr	Ala	Glu	Arg	His	Gly	Arg	Val	Val	Lys
				50						55				60	
Val	Lys	Arg	Ala	Glu	Lys	Val	Lys	Lys	Lys	Phe	Leu	Gly	Arg	Ser	Val
65						70					75				80
Glu	Val	Trp	Val	Leu	Tyr	Phe	Thr	His	Pro	Gln	Asp	Val	Pro	Ala	Ile
						85					90				95
Arg	Asp	Lys	Ile	Arg	Lys	His	Pro	Ala	Val	Ile	Asp	Ile	Tyr	Glu	Tyr
						100					105				110
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro
						115					120				125
Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Leu	Met	Ser	Phe	Asp	Ile	Glu	Thr
						130					135				140
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Gly	Thr	Gly	Pro	Ile	Leu	Met	Ile
145							150					155			160

Ser	Tyr	Ala	Asp	Glu	Ser	Glu	Ala	Arg	Val	Ile	Thr	Trp	Lys	Lys	Ile	
				165					170					175		
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Thr	Glu	Lys	Glu	Met	Ile	Lys	
				180					185					190		
Arg	Phe	Leu	Arg	Val	Val	Lys	Glu	Lys	Asp	Pro	Asp	Val	Leu	Ile	Thr	
				195					200					205		
Tyr	Asn	Gly	Asp	Asn	Phe	Asp	Phe	Ala	Tyr	Leu	Lys	Lys	Arg	Cys	Glu	
				210					215					220		
Lys	Leu	Gly	Val	Ser	Phe	Thr	Leu	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	
				225					230					235		
Ile	Gln	Arg	Met	Gly	Asp	Arg	Phe	Ala	Val	Glu	Val	Lys	Gly	Arg	Val	
				245					250					255		
His	Phe	Asp	Leu	Tyr	Pro	Val	Ile	Arg	Arg	Thr	Ile	Asn	Leu	Pro	Thr	
				260					265					270		
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Val	Phe	Gly	Lys	Pro	Lys	Glu	
				275					280					285		
Lys	Val	Tyr	Ala	Glu	Glu	Ile	Ala	Thr	Ala	Trp	Glu	Thr	Gly	Glu	Gly	
				290					295					300		
Leu	Glu	Arg	Val	Ala	Arg	Tyr	Ser	Met	Glu	Asp	Ala	Arg	Val	Thr	Tyr	
				305					310					315		
Glu	Leu	Gly	Arg	Glu	Phe	Phe	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu	
				325					330					335		
Ile	Gly	Gln	Gly	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	
				340					345					350		
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala	
				355					360					365		

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr  
370 375 380

Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile  
385 390 395 400

Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His  
405 410 415

Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp  
420 425 430

Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe  
435 440 445

Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys  
450 455 460

Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp  
465 470 475 480

Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr  
485 490 495

Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser  
500 505 510

Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu  
515 520 525

Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu  
530 535 540

His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala  
545 550 555 560

Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu  
565 570 575

Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys

580	585	590	
Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu			
595	600	605	
Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala			
610	615	620	
Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val			
625	630	635	640
Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro			
645	650	655	
Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp			
660	665	670	
Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala			
675	680	685	
Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu			
690	695	700	
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe			
705	710	715	720
Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln			
725	730	735	
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys			
740	745	750	
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp			
755	760	765	
Leu Lys Pro Lys Gly Lys Lys Lys (SEQ ID NO: 10)			
770	775		

## --Nucleotide sequence of JDF-3 DNA polymerase (Sequence 1 of WO 01/32887)

atgatccttg acgttgatta catcacccgag aatggaaagc ccgtcatcag ggtcttcaag	60
aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg	120
ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc	180
agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg	240
gaggtctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata	300
aggaagcacc ccgcggtcat cgacatctac gagtacgaca tacccttcgc caagcgctac	360
ctcatagaca agggcctaata cccgatggaa ggtgaggaag agcttaaact catgtccttc	420
gacatcgaga cgctctacca cgagggagaa gagtttgaa ccgggccgat tctgatgata	480
agctacgccg atgaaagcga ggcgcgcgtg ataacctgga agaagatcga ccttccttac	540
gttgagggtg tctccaccga gaaggagatg attaagcgct tcttgagggt cgtaaggag	600
aaggacccgg acgtgctgat aacatacaac ggcgacaact tcgacttcgc ctacctgaaa	660
aagcgctgtg agaagcttg cgtgagcttt accctcgga gggacgggag cgagccgaag	720
atacagcgca tgggggacag gtttgcggtc gaggtgaagg gcagggtaca cttcgacctt	780
tatccagtca taaggcgcac cataaacctc ccgacctaca cccttgaggc tgtatacgag	840
gcggttttcg gcaagcccaa ggagaaggtc tacgccgagg agatagccac cgctgggag	900
accggcgagg ggcttgagag ggtcgcgcgc tactcgatgg aggacgcgag ggttacctac	960
gagcttgga gggagttctt cccgatggag gccagcttt ccaggctcat cggccaaggc	1020
ctctgggacg tttcccgtc cagcaccggc aacctcgtcg agtggttcct cctaaggaag	1080
gcctacgaga ggaacgaact cgctcccaac aagcccgcg agaggagct ggcgaggaga	1140
agggggggct acgccggtgg ctacgtcaag gagccggagc ggggactgtg ggacaatatc	1200
gtgtatctag actttcgtag tctctaccct tcaatcataa tcaccacaa cgtctcgcca	1260
gatacgctca accgcgaggg gtgtaggagc tacgacgttg ccccgaggt cggtcacaag	1320
ttctgcaagg acttccccgg cttcattccg agcctgctcg gaaacctgct ggaggaaagg	1380
cagaagataa agaggaagat gaaggcaact ctcgacccgc tggagaagaa tctcctcgat	1440
tacaggcaac gcgccatcaa gattctcgcc aacagctact acggctacta cggctatgcc	1500
agggcaagat ggtactgcag ggagtgcgcc gagagcgta cggcatgggg aaggagtag	1560

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atcgaaatgg tcatcagaga gcttgaggaa aagttcggtt ttaaagtcct ctatgcagac 1620
acagacggtc tccatgccac cattcctgga gcggacgctg aaacagtcaa gaaaaaggca 1680
atggagttct taaactatat caatcccaaa ctgcccggcc ttctcgaact cgaatacgag 1740
ggcttctacg tcaggggctt cttcgtcacg aagaaaaagt acgcggtcat cgacgaggag 1800
ggcaagataa ccacgcgcgg gcttgagata gtcaggcgcg actggagcga gatagcgaag 1860
gagacgcagg cgagggtttt ggaggcgata ctcaggcacg gtgacgttga agaggccgtc 1920
agaattgtca gggaagtcac cgaaaagctg agcaagtacg aggttccgcc ggagaagctg 1980
gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta 2040
gccatagcga agcgtttggc cgccagaggt gttaaaatcc ggcccggaac tgtgataagc 2100
tacatcgttc tgaagggctc cggaaggata ggcgacaggg cgattccctt cgacgagttc 2160
gacccgacga agcacaagta cgatgcggac tactacatcg agaaccaggt tctgccggca 2220
gttgagagaa tcctcagggc cttcggctac cgcaaggaag acctgcgcta ccagaagacg 2280
aggcaggtcg ggcttggcgc gtggctgaag ccgaagggga agaagaagtg a 2331 (SEQ ID NO: 11)
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